

In re I.A. No.: PCT/NL99/00743
In re Serial No.: 09/857,408 (Nationalized)

Please amend claim 4 as follows:

4. (Amended) The array according to claim 1 in which the density of the different nucleic acid sequences bound to the carrier is in the range of 1-100,00 different sequences/cm².

Please amend claim 5 as follows:

5. (Amended) The array according to claim 1 in which restriction fragment sequences present in the nucleic acid sequences bound to the carrier have a size of 10 to 1200 nucleotides, and optionally include partial nucleotide sequences obtained by restricting the restriction fragments generated from the starting genomic DNA and/or cDNA with one or more further restriction enzymes, and/or *de novo* synthesized oligonucleotides based thereon and/or derived thereof.

Please amend claim 6 as follows:

6. (Amended) The array according to claim 1 in which the restriction fragments have been derived from genomic DNA, and in which at least 50% of the nucleic acid sequences bound to the carrier comprise the sequence of a restriction fragment that corresponds to an AFLP-marker.

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Please amend claim 7 as follows:

7. (Amended) The array according to claim 6, comprising a plurality of AFLP-markers taken from a single individual or from a group of related individuals.

Please amend claim 8 as follows:

8. (Amended) The array according to claim 6, comprising several sets of AFLP-markers, in which each set comprises one or more markers taken from a single individual, wherein said sets of one or more markers have been taken from individuals belonging to a group of related individuals.

Please amend claim 9 as follows:

9. (Amended) The array according to claim 6 in which the AFLP-markers have been taken from individuals belonging to the same species of plant, animal or microorganism.

Please amend claim 10 as follows:

10. (Amended) The array according to claim 7 in which the AFLP-markers have been taken from, or are representative for, different subspecies, varieties, cultivars or races of the same species.

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Please amend claim 11 as follows:

11. (Amended) The array according to claim 9, in which the AFLP-markers have been taken from plants selected from the group consisting of wheat, barely, maize, tomato, pepper, lettuce and rice.

Please amend claim 12 as follows:

12. (Amended) The array according to claim 6 in which AFLP-markers have been taken from the human genome.

Please amend claim 13 as follows:

13. (Amended) The array according to claim 12, in which the AFLP-markers are representative for the presence, the absence or the state of a genetically determined or influenced disease.

Please amend claim 14 as follows:

14. (Amended) The array according to claim 1 in which the restriction fragments have been generated from one or more cDNAs.

Please amend claim 15 as follows:

15. (Amended) Method for providing an array of nucleic acid sequences bound to a carrier comprising the steps

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of:

- Sub D*
- a) identifying an AFLP-marker;
 - b) providing a nucleic acid sequence that comprises a restriction fragment sequence corresponding to said AFLP-marker;
 - c) attaching the nucleic acid sequence to the carrier; and
 - d) repeating steps a) to c) for different AFLP markers to build up an array.

Please amend claim 16 as follows:

16. (Amended) The method according to claim 15, comprising the steps of:

- B*
- a) identifying a polymorphic band in an AFLP-fingerprint;
 - b) isolating a nucleic acid sequence from said polymorphic band;
 - c) optionally further amplifying, purifying and/or modifying the nucleic acid sequence; and
 - d) attaching the nucleic acid sequence to the carrier;
 - e) repeating steps a) to d) for different polymorphic bands to build up an array.

Please amend claim 17 as follows:

Sub D2

17. (Amended) A method for providing an array of nucleic acid sequences bound to a carrier comprising the steps

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of:

- Sub D2*
- a) providing a nucleic acid sequence that comprises at least one restriction fragment that has been derived from at least one cDNA
 - b) attaching the nucleic acid sequence to the carrier; and
 - c) repeating steps a) and b) for different cDNA-derived restriction fragments to build up an array.

Please amend claim 18 as follows:

18. (Amended) The method according to claim 17, comprising the steps of:

- B1*
- a) analysing at least one cDNA using AFLP-methodology to provide a cDNA-AFLP fingerprint, said fingerprint comprising at least one band;
 - b) isolating from at least one of said bands at least one nucleic acid sequence;
 - c) optionally further amplifying, purifying and/or modifying the nucleic acid sequence;
 - d) attaching the nucleic acid sequence to the carrier; and
 - e) repeating steps a) to d) for different bands and/or for different cDNAs to build up an array.

Please amend claim 19 as follows:

19. (Amended) An array, obtained by the method of

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claim 15.

Please amend claim 20 as follows:

20. (Amended) Method for analysing a nucleic acid sequence or a mixture of nucleic acids sequences, comprising contacting said nucleic acid or mixture under hybridizing conditions with an array according to claim 1.

Please amend claim 21 as follows:

21. (Amended) The method according to claim 20, in which the nucleic acid sequence or mixture is suspected to comprise at least one sequence that corresponds to a restriction fragment sequence present in the nucleic acid sequences present in the array.

Please amend claim 22 as follows:

22. (Amended) The method according to claim 20 in which the nucleic acid sequence or mixture comprises DNA.

Please amend claim 23 as follows:

23. (Amended) The method according to claim 20 in which the nucleic acid sequence or mixture comprises a mixture of restriction fragments obtained by restricting a genomic DNA with the same frequent cutter restriction enzyme and rare

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cutter restriction enzyme as used in generating the
restriction fragment sequences present in the array.

Please amend claim 24 as follows:

24. (Amended) The method according to claim 20 in
which the mixture of restriction fragments contacted with the
array has been amplified prior to hybridisation with the
array.

Please amend claim 25 as follows:

25. (Amended) The method according to claim 23 in
which the mixture of restriction fragments has been amplified
using AFLP.

Please amend claim 26 as follows:

26. (Amended) The method according to claim 2 in
which the nucleic acid sequence or mixture of nucleic acid
sequences contacted with the array has been derived from an
individual related to the individual(s) from which the AFLP-
markers present in the array have been taken.

Please amend claim 27 as follows:

27. (Amended) The method according to claim 26, in
which the individual from whom the nucleic acid sequence or

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mixture of nucleic acid sequences has been derived belongs to the same species as the individual(s) from which the AFLP-marker(s) present in the array have been taken.

Please amend claim 28 as follows:

28. (Amended) The method according to claim 27 wherein an array is used to analyze a nucleic acid sequence or a mixture of nucleic acid sequences derived from plants selected from the group consisting of wheat, barley, maize, tomato, pepper, lettuce, and rice;

wherein the array comprises a carrier and at least two different nucleic acid sequences bound to said carrier, wherein each of the nucleic acid sequences comprises at least one nucleic acid sequence that corresponds to the sequence of a restriction fragment obtained by restricting at least one member of the group consisting of a genomic DNA and at least one cDNA with at least one frequent cutter restriction enzyme and at least on rare cutter restriction enzyme;

wherein the restriction fragments have been derived from genomic DNA in which at least 50% of the nucleic acid sequences bound to the carrier comprise the sequence of a restriction fragment that corresponds to an AFLP-marker taken from individuals belonging to the same species of plant.

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Please amend claim 29 as follows:

29. (Amended) Kit of parts comprising an array according to claim 1 and optionally other components for use with the array selected from the group consisting of restriction enzymes, polymerase(s), adapters, primers, buffers, nucleotides, labels and other detection agents, containers/packaging and manuals.

Please amend claim 30 as follows:

30. (Amended) Non-processed or processed results or data obtainable by analysing a nucleic acid or mixture of nucleic acids with an array according to claim 1 in the form of an image, of a score, of digital or analog data, optionally stored on a suitable data carrier.

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REMARKS

The present Preliminary Amendment is submitted in order to eliminate multiple dependencies. No limitations are included in the amendment, and none are intended.

In view of the above, it is respectfully submitted that the claims are now in condition for examination, and prompt and favorable consideration are earnestly solicited.

Respectfully submitted,

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